ELabELN | Template Use Case White Paper

RNA-Seq Experiment Template

Structured Documentation for Bulk RNA Sequencing — From RNA QC and the Cohort Sample Sheet Through DESeq2 Differential Expression

APPLIES TO

- Academic and life sciences research laboratories
- Biotechnology and pharmaceutical R&D groups
- Genomics and sequencing core facilities
- Genetics / genomics labs and contract research organizations (CROs)

RELEVANT COMPLIANCE & INTEGRITY FRAMEWORKS

- FDA 21 CFR Part 11 — Electronic records and signatures
- EU Annex 11 — Computerized systems in regulated environments
- GAMP 5 — Software validation for regulated industries
- NIH / NSF reproducibility and FAIR data-management requirements

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1. Executive Summary

A differential-expression study lives or dies on its sample sheet. Which sample belongs to which group, which biological replicate, and which index — that mapping is the single thread that ties a fold change back to real biology, and it is the easiest thing in the entire workflow to get wrong. An RNA-Seq cohort also spans two very different worlds: a wet lab that extracts RNA, builds libraries, and sequences, and a computational side that aligns, quantifies, and tests for differential expression using a specific chain of tool versions. When the sample sheet is a spreadsheet passed between those two worlds and the pipeline versions live in a analyst's shell history, the study becomes impossible to reproduce and a mislabeled sample or an unrecorded reference-genome version can silently invert a result.

The ELabELN RNA-Seq Experiment Template solves this by providing a pre-built, fully structured cohort record that loads from the template library in a single click. It ships with a 10-step protocol, validated library-prep references, a pre-wired cohort sample sheet, and typed inputs for RIN, library yields, fragment sizes, index sequences, expected read depth, sequencer parameters, and the downstream analysis pipeline. Library-prep kits, sequencing reagents, and index sets link to the ELabELN inventory, and the tamper-evident audit trail captures every sample sheet, every library QC, and every analysis run.

This white paper describes what the template contains, the transcriptomics use case it is designed to support, the upstream and downstream workflows it connects to, the benefits it delivers to the team, and how a laboratory can deploy it and begin running cohorts within days.

> **KEY BENEFIT**
> Labs that adopt the RNA-Seq template stop rebuilding the sample sheet and run notes every cohort and losing the sample-to-group mapping between the bench and the pipeline, capture kit-lot, index-pool, and pipeline-version provenance automatically, and gain a queryable, cross-cohort record — one place that ties every differentially expressed gene back to its sample sheet, its parameters, and the analyst who produced it.

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2. What Is Bulk RNA-Seq, and Why Does Documentation Matter?

2.1 The Technique

Bulk RNA sequencing measures the expression of every gene in a sample by converting its RNA into a sequencing library, reading millions of short fragments on a high-throughput sequencer, and computationally mapping those reads back to a reference genome to count how many originated from each gene. In a differential-expression study, a cohort of samples spanning two or more conditions is processed together: total RNA is quality-checked (RIN), libraries are prepared and QC'd, samples are pooled with unique indices and sequenced, and the resulting reads are demultiplexed, aligned, quantified, and tested for genes whose expression differs between groups. The comparison is only meaningful if the whole cohort is processed consistently and every sample's group assignment is correct.

This is the standard approach for differential expression, transcriptomic profiling, and biomarker discovery. Its power is genome-wide, quantitative resolution; its difficulty is that a cohort passes through many stages and two teams, and the result is exquisitely sensitive to two things: the integrity of the sample sheet, and the exact bioinformatics pipeline — the reference-genome build, the aligner, the quantifier, and the differential-expression method, each at a specific version. A batch effect, a swapped index, or an unrecorded tool version can produce a result that looks clean and is wrong.

Because an RNA-Seq result is the product of a cohort processed across two teams and a versioned pipeline, **the sample sheet, the run parameters, and the analysis versions are what make a study reproducible and comparable to the next cohort — which is exactly why they must live in one structured record rather than a spreadsheet handed between the bench and the terminal.**

2.2 The Documentation Problem

Recording an RNA-Seq cohort across spreadsheets, a sequencer, and analysts' notes creates a set of interconnected risks:

- The sample sheet — the sample-to-group, replicate, and index mapping — is kept in a spreadsheet that can be separated from the data, mislabeled, or edited without a trace, silently corrupting the comparison.
- Library QC (RIN, yield, fragment size) is jotted per sample and never assembled, so an outlier library that will skew the cohort is not caught.
- Kit lot, sequencing-reagent lot, and index pool are not captured against the cohort, so a batch effect cannot be traced to a reagent.
- The bioinformatics pipeline — reference-genome build, aligner, quantifier, and DE-method versions — lives with the analyst, disconnected from the wet-lab record, so the analysis cannot be reproduced.
- Because the workflow spans two teams, there is no single timestamped, attributed record of who did the wet-lab work and who ran the analysis.
- Prior cohorts cannot be retrieved to compare pipeline versions or check for batch effects across a shared resource.

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These are the gaps that make RNA-Seq studies hard to reproduce and compare, and they are the gaps this template was designed to close.

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3. Template Overview: What Ships with the Template

The ELabELN RNA-Seq Experiment Template is a pre-populated experiment record available to all ELabELN subscribers directly from the template library. It ships configured for a bulk RNA sequencing differential-expression study, with a 10-step protocol covering total RNA QC through STAR alignment, featureCounts quantification, and DESeq2 differential expression. The default configuration assumes a polyA-selected, strand-specific library prep (NEBNext Ultra II Directional RNA Library Prep Kit), Illumina NextSeq 2000 sequencing with a P2 100-cycle paired-end kit, and a Snakemake-orchestrated alignment and DE analysis — with a 24-sample cohort (HER2 siRNA knockdown vs scrambled control across three breast cancer cell lines) as the worked example. Every section is editable — the configuration is a tested baseline, not a locked format.

3.1 Template Sections at a Glance

The template populates the existing ELabELN experiment sections your lab already works in. Your team edits a working baseline instead of rebuilding the sample sheet and run notes from scratch every cohort.

Section	What it pre-populates
Main Text	Study-design summary, library-prep notes, and expected DEG results, authored in the TinyMCE rich-text editor and linked to the upstream RNA extraction.
Extra Fields	Twelve structured, typed fields grouped as Sample, Library, and Sequencing Run — sample group, biological replicate, RIN, library concentration, average fragment size, index sequence, expected read depth, sequencer instrument and kit, and paired-end length. Typed values make sample sheets and run parameters queryable across cohorts.
Steps	A 10-step workflow checklist covering RNA QC through DESeq2 DEG analysis. Each tick is timestamped to the audit trail, and the sequencer run is auto-logged.
Compounds	The library-prep kit, sequencing kit, index sets, and RNA-Seq controls pre-linked from the compound database, with kit lots carried in automatically and index-pool tracking inline.
Links & Resources	Pre-wired to the lab's NEBNext Ultra II SOP, the bioinformatics Snakemake DEG workflow, and the GRCh38 reference genome.
Storage & Files	−80 °C RNA and prepped-library aliquot storage, plus labelled attachment slots for raw FASTQ paths and DESeq2 result files (CSV + HTML report).

Main Text
Study design summary, library-prep notes, expected DEG results.
Extra Fields
Typed: group, replicate, RIN, library conc, index, depth, instrument, PE.
Steps
10-step checklist; each tick timestamped, sequencer run logged.
Compounds
Library-prep kit, sequencing kit, index sets, RNA-Seq controls from inventory.
Links & Resources
NEBNext Ultra II SOP, Snakemake DEG workflow, GRCh38 reference genome.
Storage & Files
−80 °C RNA + library aliquots; FASTQ paths + DESeq2 results (CSV + HTML).

Figure 1. The six ELabELN experiment sections pre-populated by the RNA-Seq template.

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3.2 The 10-Step Protocol

The workflow checklist is the operational spine of the template. Each step maps to a discrete wet-lab, sequencing, or computational action and writes a timestamped, user-attributed entry to the audit trail when checked off. The sequencer run is auto-logged, and the alignment and differential-expression steps are performed in an external pipeline, with their versions and results recorded as typed fields.

Step	Action	What it captures
1	RNA QC (RIN)	RNA integrity number
2	Library prep	Library-prep chemistry
3	Library QC	Library concentration; average fragment size
4	Pool & index	Index sequence; index pool
5	Sequence (NextSeq, PE)	Instrument & kit; PE length; expected depth (auto-logged)
6	Demultiplex	FASTQ generation
7	QC & trim	Read QC and trimming
8	Align (STAR)	Aligner version; reference genome (external)
9	Quantify (featureCounts)	Quantifier; count matrix
10	Differential expression (DESeq2)	DE method; top DEGs; e-signature

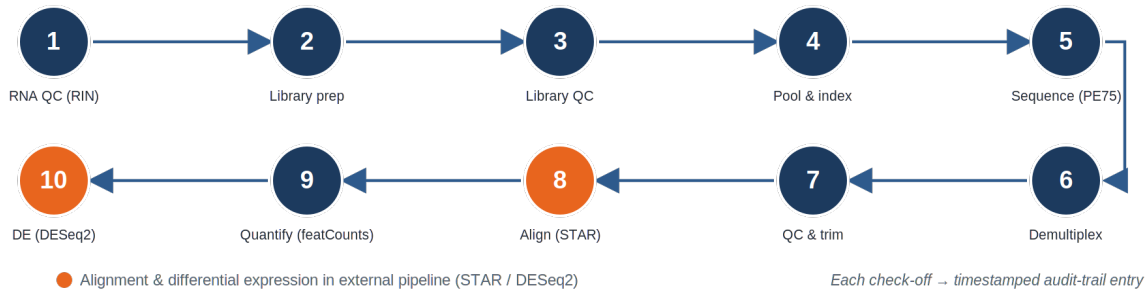

Figure 2. The 10-step bulk RNA-Seq workflow — orange steps are the alignment and differential expression performed in an external pipeline (STAR / DESeq2); every check-off writes a timestamped entry to the ELabELN audit trail.

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4. The Use Case: When and How the Template Is Used

The template is intended as a tested baseline for academic and life sciences labs running differential-expression and transcriptomic studies. It is configured around a recognizable reference — a bulk RNA-Seq knockdown-versus-control cohort — but the scenarios it serves span the transcriptomics bench and its downstream analysis.

4.1 Differential Expression (Primary Use Case)

The core scenario: comparing gene expression between conditions across a cohort. The template captures the sample sheet, the library QC, the run parameters, and the top differentially expressed genes in one structured record, so a result is fully reconstructable — which samples, which pipeline, which versions — rather than a gene list detached from the cohort that produced it.

4.2 Transcriptomic Profiling

Profiling studies characterize expression across tissues, conditions, or time without a single fixed contrast. The template's typed sample sheet and run fields structure the cohort so profiles are comparable and queryable across samples.

4.3 Biomarker Discovery

Discovery cohorts screen for expression signatures. Because the sample sheet and results are structured and queryable, candidate signatures can be traced back to their exact samples and pipeline, and compared across cohorts as the study scales.

4.4 Time-Course and Multi-Condition Designs

More complex designs — time courses, multiple conditions, factorial layouts — depend even more on an accurate sample sheet. The template's structured group and replicate fields capture the design so the analysis model matches the biology.

4.5 Cross-Cohort and Pipeline-Version QC

Because sample sheets, run parameters, and pipeline versions are captured together, the template doubles as a running QC record across cohorts. A lab can pull every cohort run under a reference-genome build or pipeline version and compare library QC, read depth, and results — the objective basis for detecting a batch effect or a pipeline change before it confounds a conclusion.

4.6 Wet-Lab and Bioinformatics Teams, and CROs

RNA-Seq inherently spans two teams. Because every ELabELN edition includes unlimited users, the PI, wet-lab postdocs, computational analysts, and rotating collaborators can all work from the same record. Granular permissions let the PI control who can edit the wet-lab sections versus the bioinformatics sections — the role separation a core facility or CRO needs so each side owns its stage of the record without overwriting the other's.

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5. Dependencies and Connected Workflows

The RNA-Seq template does not exist in isolation. It sits inside a network of connected workflows — upstream, parallel, external, and downstream — that give the cohort record its full scientific and provenance value.

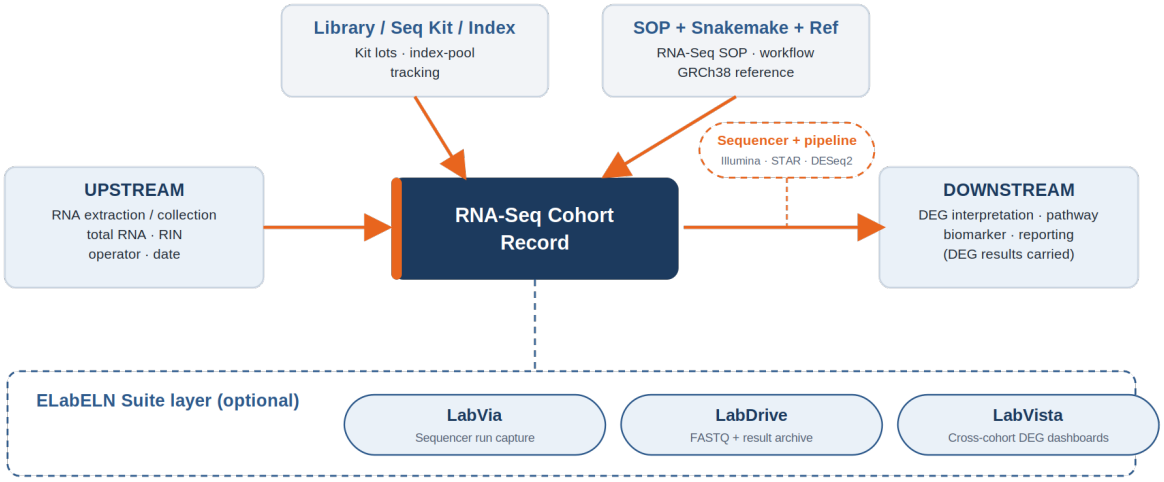

Figure 3. The template connects an upstream RNA extraction, parallel inventory and SOP/workflow/reference systems, the external sequencer-and-pipeline stack, and downstream interpretation and reporting workflows.

5.1 Upstream: RNA Extraction and Collection

Every cohort begins with extracted RNA. The template links to the upstream RNA-extraction record, so opening a cohort surfaces the sample source, the RIN, and the operator and date, anchoring every library and every read back to the RNA it came from — and connecting directly to the lab's RNA-extraction workflow.

5.2 Parallel: Library-Prep, Sequencing, and Index Inventory

The Compounds section links the library-prep kit, sequencing kit, index sets, and RNA-Seq controls directly to the ELabELN inventory. Because kit lots and index pools drive comparability and demultiplexing, this traceability is decisive. Through the link the record automatically carries:

- **Kit lots, carried automatically**, so a batch effect can be traced to a specific library-prep or sequencing lot.
- **Index-pool tracking, shown inline**, so index collisions across pooled samples are caught before sequencing.
- **Expiry and stock levels**, with low-stock warnings before a run, so a cohort is not started against a depleted or expired kit.

Barcode and QR scanning can populate these links from the physical kit, keeping lot capture effortless across a multi-sample prep.

5.3 Parallel: SOPs, the Snakemake Workflow, and the Reference Genome

The Links section connects the cohort to the lab's version-controlled RNA-Seq SOP, the bioinformatics Snakemake DEG workflow, and the GRCh38 reference genome. Because these

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are version-controlled in ELabELN, every cohort records exactly which SOP, workflow, and reference build it used — the anchors that reproducibility and cross-cohort comparison depend on.

5.4 External: The Sequencer and Bioinformatics Pipeline

The Illumina sequencer produces the raw reads, and the bioinformatics pipeline — STAR alignment, featureCounts quantification, and DESeq2 differential expression, orchestrated by Snakemake or Nextflow — turns them into results. ELabELN captures the analysis parameters and result references rather than running the analysis itself: the reference-genome version, aligner, quantifier, and DE-method versions are recorded as typed fields; the cohort sample sheet and a top-DEG summary live in the spreadsheet editor; and the raw FASTQ paths, the count matrix, the DE results table, and the HTML report attach to the record. The sample sheet, the run, and the interpreted result stay together in one place.

5.5 Downstream: Interpretation, Pathway Analysis, and Cross-Cohort

The differential-expression results feed pathway analysis, biomarker interpretation, and reporting, and — because the sample sheets, parameters, and results are typed and queryable — cross-cohort analysis across a shared transcriptomic resource. A batch effect or a pipeline change shows up when cohorts are compared, not after a conclusion is drawn.

5.6 The ELabELN Suite: Instruments and Dashboards

Everything above is available in ELabELN Standard. Labs on the ELabELN Suite gain three layers that connect to the same record: LabVia captures run data directly from the sequencer; LabDrive adds metadata search, versioning, and role-based access across FASTQ and result-file archives; and LabVista builds cross-cohort differential-expression dashboards on the structured sample-sheet and result metadata. The same audit trail and data-integrity controls span all layers.

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6. How the Team Benefits

The template is built to deliver value across both halves of the workflow, not just at the bench. The benefits compound with every cohort a lab runs.

6.1 Start From a Tested Baseline, Not a Blank Sample Sheet

The scaffold — protocol, typed fields, sample sheet, reagent links, SOP, Snakemake workflow, and reference genome — is already built. The team edits a working configuration to match the study they actually run, rather than rebuilding the sample sheet and run notes from scratch every cohort. The first cohort is faster, and every subsequent one is consistent with it.

6.2 Document by Doing, Across Both Teams

Checking off each of the 10 steps as it happens produces a contemporaneous, timestamped record as a by-product of the work, and the sequencer run is auto-logged. Wet-lab prep, sequencing, and analysis are documented as they occur, by whoever performs them — with no separate write-up to reconstruct later.

6.3 Never Lose the Sample Sheet or Lot Provenance Again

Because the sample sheet is a structured artifact and the kits and indices are linked to inventory, the sample-to-group mapping, kit lots, and index pools are captured permanently on every cohort. When a result is questioned, the sample sheet and provenance are on the record — closing the most consequential RNA-Seq gap by default.

6.4 Cross-Cohort Comparisons You Can Query

Typed sample-sheet, run, and pipeline-version fields make the study queryable. A team can pull every cohort run under a reference build or pipeline version, compare library QC and results, and catch a batch effect or a pipeline change early — instead of discovering it after the study is assembled.

6.5 Audit-Ready Records with Role Separation

The tamper-evident audit trail, version-controlled linkage, electronic signatures, and granular permissions mean the record that results from normal use is already structured to support cohort-level reproducibility documentation, multi-PI collaboration on shared transcriptomic resources, and FDA 21 CFR Part 11 review when the lab's quality system requires it — with the wet lab and the bioinformatics team each owning their stage of the record.

> **AT THE BENCH, IN PRACTICE**
>
> A wet-lab postdoc opens the template, enters the cohort sample sheet as a structured table, scans the library-prep and sequencing kits to capture their lots, and checks off RNA QC, library prep, and pooling as the RIN and library yields go into typed fields. The sequencer run auto-logs the instrument and read depth. The computational analyst then records the reference build, STAR and DESeq2 versions, and the Snakemake workflow, and attaches the count matrix and DE results with the top DEGs. Months later, comparing cohorts, the PI queries every cohort on that pipeline version and sees whether the results hold — and whether any sample sat apart on the PCA.

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7. The Sample Sheet and Cohort Structure

7.1 The Default Reference: A Knockdown-vs-Control Cohort

The template ships configured for a bulk RNA-Seq differential-expression study: a 24-sample cohort comparing HER2 siRNA knockdown against scrambled control across three breast cancer cell lines, with polyA-selected strand-specific libraries, paired-end sequencing on an Illumina NextSeq 2000, and a Snakemake-orchestrated STAR / featureCounts / DESeq2 pipeline against the GRCh38 reference. The sample sheet maps every sample to its group, cell line, and index, and a post-analysis principal-component plot confirms that the cohort separates by condition before any gene-level result is trusted. This concrete reference demonstrates the full sample-sheet-to-result workflow out of the box; swap the study design, library chemistry, or pipeline to match what your lab runs.

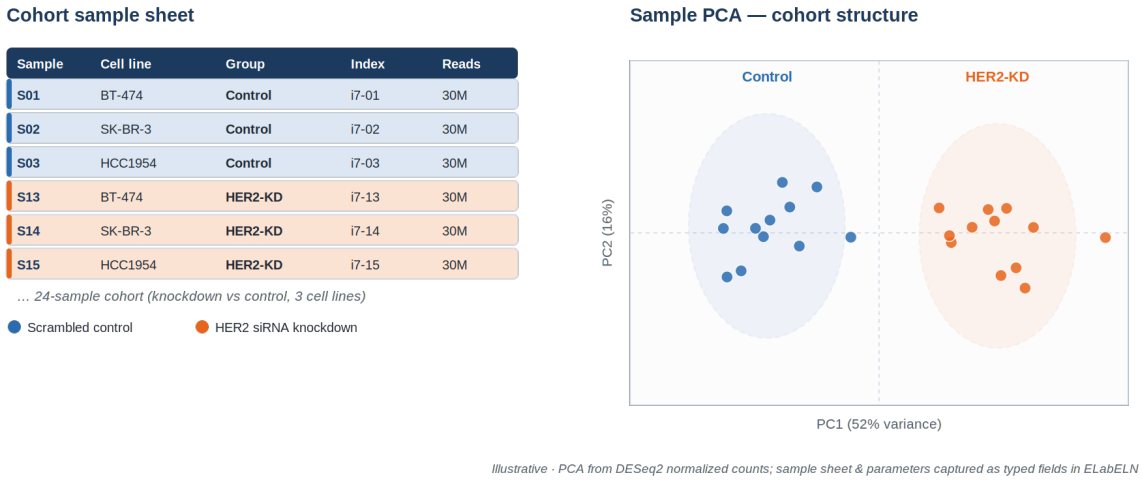

Figure 4. The cohort sample sheet alongside a sample PCA confirming that the cohort separates by condition. Illustrative; the PCA comes from the DESeq2-normalized counts, and the sample sheet and parameters are captured as typed fields in ELabELN.

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7.2 How the Template Handles the Sample Sheet, Parameters, and Results

The sample group, biological replicate, RIN, library concentration, fragment size, index sequence, expected depth, and sequencer parameters are all captured as typed fields, and the cohort sample sheet plus a top-differentially-expressed-genes summary live in the spreadsheet editor. The analysis parameters and result references — reference-genome version, aligner (STAR), quantifier (featureCounts, Salmon, kallisto), and DE method (DESeq2, edgeR, limma-voom) — are recorded as typed fields, with the count matrix, normalized counts, DE results table, and HTML report attached as files. Because the sample sheet and pipeline versions are structured and queryable, cross-cohort comparison is straightforward: query every cohort run under a pipeline version or reference build and review library QC and results side by side.

Element	Default configuration	Editable to
Study design	Case vs control (knockdown vs scrambled)	Time course, multi-condition, factorial
Library chemistry	polyA-selected, strand-specific	Total RNA + rRNA depletion, small RNA, 3′-only, exome capture
Platform	Illumina NextSeq 2000 (PE)	NovaSeq, MiSeq, MGI DNBSEQ
Pipeline	STAR / featureCounts / DESeq2 (Snakemake)	Salmon, kallisto; edgeR, limma-voom; Nextflow
Scope	Bulk RNA-Seq	Single-cell (dedicated template)

Figure 5. The template's default configuration — fully editable for any study design, library chemistry, platform, or analysis pipeline.

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8. Configuring the Template for Your Study

Adapting the template to a different design or chemistry is a matter of editing the relevant sections — not rebuilding the structure.

8.1 Change the Study Design

Reshape the cohort for your comparison — case versus control, a time course, or a multi-condition design — by editing the sample-sheet group and replicate fields so the analysis model matches the biology.

8.2 Swap the Library Chemistry

Change the library-prep chemistry (polyA selection, total RNA with rRNA depletion, small RNA, 3′-only, exome capture) by editing the library section. If the kits already exist in the ELabELN compound database, simply re-link them; their lots flow in automatically.

8.3 Change the Platform and Pipeline, and Bulk vs. Single-Cell

Switch the sequencing platform (NextSeq, NovaSeq, MiSeq, MGI DNBSEQ), adjust the read length and paired-end configuration, and change the downstream pipeline (aligner, quantifier, DE method). Moving from bulk to single-cell is best handled by a dedicated single-cell template, which the ELabELN team can scaffold during onboarding.

8.4 Save a Custom Version

Once configured, save your edits as a private template scoped to your lab, or publish back to the ELabELN template library. Every subsequent cohort opens from your configured, version-controlled design, and separate versions can be maintained for different study types, chemistries, or platforms.

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9. Getting Started

ELabELN Standard is a cloud-hosted SaaS deployment typically live within one to two business days of account creation. There is no hardware to buy, no IT project, and no per-seat licensing.

1. **Start an ELabELN account.** Visit elabeln.com/get-started. ELabELN Standard runs on LabLynx's managed cloud infrastructure.
2. **Provision your instance.** LabLynx provisions the instance within one to two business days; you receive a URL, admin credentials, and onboarding documentation.
3. **Load the RNA-Seq template.** From the template library, select the RNA-Seq template and click “Use This Template.” An editable instance opens immediately.
4. **Add your kits, reagents, and indices to the inventory.** Enter your library-prep and sequencing kits, index sets, and controls with lot numbers and −80 °C storage locations. This is a one-time setup step.
5. **Link your SOP, Snakemake workflow, and reference genome.** Upload your RNA-Seq SOP, connect the bioinformatics Snakemake workflow, and link the reference-genome build to the template's Links section.
6. **Customize the template for your study.** Edit the study design and sample sheet, the library chemistry, the platform, and the analysis pipeline, then save as a private team version.
7. **Run your first cohort.** Open your saved template, complete the 10-step checklist across the wet lab and bioinformatics, attach the FASTQ paths and DE results, and have the PI sign off electronically.

TYPICAL TIMELINE

Day 1: Account requested at elabeln.com/get-started. Day 2–3: Instance provisioned; kit/index inventory populated; SOP, Snakemake workflow, and reference genome linked. Day 3–4: Template configured and saved as a private version for your study design. Day 4–5: First cohort documented in ELabELN with the sample sheet, library QC, and DEG results captured and an e-signature.

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9.1 ELabELN Standard vs. ELabELN Suite

Capability	Standard	Suite
RNA-Seq template access	Included	Included
Unlimited users	Included	Included
Audit trail and e-signatures	Included	Included
Library / sequencing kit / index inventory with lot tracking	Included	Included
SOP, Snakemake workflow & reference-genome linking	Included	Included
FASTQ paths + DESeq2 result attachments	Included	Included
LabVia direct sequencer run capture	—	Suite layer
LabDrive FASTQ + result archive search & versioning	—	Suite layer
LabVista cross-cohort differential-expression dashboards	—	Suite layer

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10. Frequently Asked Questions

Can I configure the template for my library chemistry and study design?

Yes. Every section is editable. Swap in different library-prep chemistries (polyA selection, total RNA with rRNA depletion, small RNA, 3′-only, exome capture), change the sequencing platform (NextSeq, NovaSeq, MiSeq, MGI DNBSEQ), adjust the read length and paired-end configuration, or change the downstream analysis pipeline. Save your edits as a private template scoped to your lab, or publish back to the ELabELN template library.

Does the template work for single-cell RNA-Seq?

This template is configured for bulk RNA-Seq. The structural pattern — sample sheet, library QC, sequencing run, alignment, quantification — carries over to single-cell, but the specific fields, library-prep chemistry (10x Chromium, BD Rhapsody, Smart-seq3, Parse), and downstream pipelines (Cell Ranger, Seurat, Scanpy) differ enough that a dedicated single-cell template is more useful. The ELabELN team can scaffold a single-cell variant during onboarding.

How does the template handle the bioinformatics analysis side?

The template captures the analysis parameters and result references rather than running the analysis itself. The Snakemake or Nextflow workspace, reference-genome version, alignment-tool version (STAR), quantifier (featureCounts, Salmon, kallisto), and DE method (DESeq2, edgeR, limma-voom) are recorded as typed fields. Result files (count matrix, normalized counts, DE results table, HTML report) attach as files. The structured record makes cross-cohort comparison of pipeline versions and parameter choices straightforward.

Is it included in every ELabELN plan?

Yes. Every published template in the ELabELN library is available to all subscribers in both the Standard and Suite editions, with unlimited users in either edition and no per-template fee.

Can my whole lab use this template?

Yes. Every ELabELN edition includes unlimited users, so the PI, wet-lab postdocs, computational analysts, and rotating collaborators can all use the template without per-seat charges. Granular permissions let the PI control who can edit the wet-lab versus the bioinformatics sections.

How quickly can my lab start running RNA-Seq cohorts in ELabELN?

ELabELN Standard cloud deployment is typically live in one to two business days. Once the instance is provisioned, the template loads from the library in a single click, with the study design, library chemistry, and analysis pipeline editable to match the cohorts your lab actually runs.

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11. Conclusion

The ELabELN RNA-Seq Experiment Template is not simply a digital version of a sample sheet. It is a structured, audit-ready, searchable record that connects to your kit and index inventory, your SOPs, Snakemake workflow, and reference genome, the RNA the cohort measured, your sequencer and bioinformatics pipeline, and the interpretation and reporting the results feed — and, in the Suite edition, cross-cohort differential-expression dashboards. It turns a study that spans two teams and a versioned pipeline into a single record whose sample sheet, parameters, and results are captured, comparable, and defensible.

For a laboratory that runs RNA-Seq regularly, the benefit compounds with every cohort. Sample sheets, run parameters, and pipeline versions accumulate into one queryable, cross-cohort history. Every kit lot and index pool is traceable. Every reference build and tool version is documented. Every stage is timestamped and attributed to whoever performed it — so a mislabeled sample or an unrecorded pipeline version can no longer break a study, and a batch effect is caught before it confounds a conclusion.

The template is available to all ELabELN subscribers today. A new instance is live in one to two business days, and the first structured cohort is typically documented within a week of account creation.

GET STARTED

Visit elabeln.com/get-started to request your ELabELN instance, or contact LabLynx at 866.522.5969 or info@lablynx.com. Load the RNA-Seq template, configure it for your study design and library chemistry, and run your next cohort from a tested, audit-ready baseline.

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